

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: \_\_\_\_\_

09/526,106B

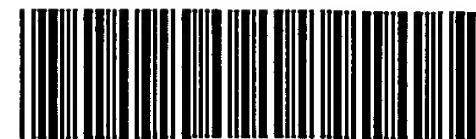
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IFW16

Date Processed by STIC: \_\_\_\_\_

08/15/2005

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 08/15/2005

PATENT APPLICATION: US/09/526,106B

TIME: 09:35:25

Input Set : A:\021167-000700US.ST25.txt

Output Set: N:\CRF4\08152005\I526106B.raw

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3 <110> APPLICANT: Balint, Robert F.
4       Her, Jeng-Horng
5       KaloBios, Inc.
7 <120> TITLE OF INVENTION: Interaction-Activated Proteins
9 <130> FILE REFERENCE: 021167-000700US
11 <140> CURRENT APPLICATION NUMBER: US 09/526,106B
12 <141> CURRENT FILING DATE: 2000-03-15
14 <150> PRIOR APPLICATION NUMBER: US 60/124,339
15 <151> PRIOR FILING DATE: 1999-03-15
17 <150> PRIOR APPLICATION NUMBER: US 60/135,926
18 <151> PRIOR FILING DATE: 1999-05-25
20 <150> PRIOR APPLICATION NUMBER: US 60/175,968
21 <151> PRIOR FILING DATE: 2000-01-13
23 <160> NUMBER OF SEQ ID NOS: 27
25 <170> SOFTWARE: PatentIn Ver. 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 789
29 <212> TYPE: DNA
30 <213> ORGANISM: Escherichia coli
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(789)
35 <223> OTHER INFORMATION: TEM-1 beta-lactamase
37 <400> SEQUENCE: 1
38 cac cca gaa acg ctg gtg aaa gta aaa gat gct gaa gat cag ttg ggt      48
39 His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
40   1               5               10               15
42 gca cga gtg ggt tac atc gaa ctg gat ctc aac agc ggt aag atc ctt      96
43 Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
44   20               25               30
46 gag agt ttt cgc ccc gaa gaa cgt ttt cca atg atg agc act ttt aaa      144
47 Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
48   35               40               45
50 gtt ctg cta tgt ggc gcg gta tta tcc cgt att gac gcc ggg caa gag      192
51 Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu
52   50               55               60
54 caa ctc ggt cgc cgc ata cac tat tct cag aat gac ttg gtt gag tac      240
55 Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
56  65               70               75               80
58 tca cca gtc aca gaa aag cat ctt acg gat ggc atg aca gta aga gaa      288
59 Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
60   85               90               95
62 tta tgc agt gct gcc ata acc atg agt gat aac act gcg gcc aac tta      336

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63 Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
64          100          105          110
66 ctt ctg aca acg atc gga gga ccg aag gag cta acc gct ttt ttg cac 384
67 Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
68          115          120          125
70 aac atg ggg gat cat gta act cgc ctt gat cgt tgg gaa ccg gag ctg 432
71 Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
72          130          135          140
74 aat gaa gcc ata cca aac gac gag cgt gac acc acg atg cct gta gca 480
75 Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala
76 145          150          155          160
78 atg gca aca acg ttg cgc aaa cta tta act ggc gaa cta ctt act cta 528
79 Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
80          165          170          175
82 gct tcc cgg caa caa tta ata gac tgg atg gag gcg gat aaa gtt gca 576
83 Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala
84          180          185          190
86 gga cca ctt ctg cgc tcg gcc ctt ccg gct ggc tgg ttt att gct gat 624
87 Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp
88          195          200          205
90 aaa tct gga gcc ggt gag cgt ggg tct cgc ggt atc att gca gca ctg 672
91 Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu
92          210          215          220
94 ggg cca gat ggt aag ccc tcc cgt atc gta gtt atc tac acg acg ggg 720
95 Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly
96 225          230          235          240
98 agt cag gca act atg gat gaa cga aat aga cag atc gct gag ata ggt 768
99 Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly
100          245          250          255
102 gcc tca ctg att aag cat tgg 789
103 Ala Ser Leu Ile Lys His Trp
104          260
107 <210> SEQ ID NO: 2
108 <211> LENGTH: 263
109 <212> TYPE: PRT
110 <213> ORGANISM: Escherichia coli
112 <220> FEATURE:
113 <223> OTHER INFORMATION: TEM-1 beta-lactamase
115 <400> SEQUENCE: 2
116 His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
117 1 5 10 15
119 Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
120 20 25 30
122 Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
123 35 40 45
125 Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu
126 50 55 60
128 Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
129 65 70 75 80

```

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```

131 Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
132      85      90      95
134 Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
135      100     105     110
137 Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
138      115     120     125
140 Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
141      130     135     140
143 Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala
144 145      150     155     160
146 Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
147      165     170     175
149 Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala
150      180     185     190
152 Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp
153      195     200     205
155 Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu
156      210     215     220
158 Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly
159 225      230     235     240
161 Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly
162      245     250     255
164 Ala Ser Leu Ile Lys His Trp
165      260
168 <210> SEQ ID NO: 3
169 <211> LENGTH: 5
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
176 <400> SEQUENCE: 3
177 Gly Gly Gly Gly Ser
178 1      5
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 15
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence:flexible linker
189 <400> SEQUENCE: 4
190 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
191 1      5      10      15
194 <210> SEQ ID NO: 5
195 <211> LENGTH: 6
196 <212> TYPE: PRT
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence:hexa-histidine
201 tag

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Input Set : A:\021167-000700US.ST25.txt

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203 <400> SEQUENCE: 5
204 His His His His His His
205 1 5
208 <210> SEQ ID NO: 6
209 <211> LENGTH: 5
210 <212> TYPE: PRT
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence:flexible linker
215 of variable length
217 <220> FEATURE:
218 <221> NAME/KEY: REPEAT
219 <222> LOCATION: (1)..(5)
220 <223> OTHER INFORMATION: (G-4S)-x, amino acids 1-5 may be repeated an
221 undefined number of times
223 <400> SEQUENCE: 6
224 Gly Gly Gly Gly Ser
225 1 5
228 <210> SEQ ID NO: 7
229 <211> LENGTH: 267
230 <212> TYPE: PRT
231 <213> ORGANISM: Escherichia coli
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Neomycin phosphotransferase II (NPTII)
236 <400> SEQUENCE: 7
237 Met Gly Ser Ala Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala
238 1 5 10 15
240 Ala Trp Val Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile
241 20 25 30
243 Gly Cys Ser Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro
244 35 40 45
246 Val Leu Phe Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln
247 50 55 60
249 Asp Glu Ala Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys
250 65 70 75 80
252 Ala Ala Val Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu
253 85 90 95
255 Leu Gly Glu Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro
256 100 105 110
258 Ala Glu Lys Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr
259 115 120 125
261 Leu Asp Pro Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile
262 130 135 140
264 Glu Arg Ala Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp
265 145 150 155 160
267 Leu Asp Glu Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg
268 165 170 175
270 Leu Lys Ala Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly
271 180 185 190

```

## RAW SEQUENCE LISTING

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TIME: 09:35:25

Input Set : A:\021167-000700US.ST25.txt

Output Set: N:\CRF4\08152005\I526106B.raw

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273 Asp Ala Cys Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly
274      195      200      205
276 Phe Ile Asp Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile
277      210      215      220
279 Ala Leu Ala Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala
280 225      230      235      240
282 Asp Arg Phe Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg
283      245      250      255
285 Ile Ala Phe Tyr Arg Leu Leu Asp Glu Phe Phe
286      260      265
289 <210> SEQ ID NO: 8
290 <211> LENGTH: 18
291 <212> TYPE: PRT
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Description of Artificial Sequence:CD40-binding
296      Trxpep
298 <400> SEQUENCE: 8
299 Cys Gly Pro Lys Glu Leu Arg Ile Gly Gly Arg Pro Arg Arg Pro Gly
300  1      5      10      15
302 Pro Cys
305 <210> SEQ ID NO: 9
306 <211> LENGTH: 18
307 <212> TYPE: PRT
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Description of Artificial Sequence:CD40-binding
312      Trxpep
314 <400> SEQUENCE: 9
315 Cys Gly Pro Glu Gly Gln Gly Gly Val Ala Val Gly Gly Val Gly Gly
316  1      5      10      15
318 Pro Cys
321 <210> SEQ ID NO: 10
322 <211> LENGTH: 16
323 <212> TYPE: PRT
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Description of Artificial Sequence:CD40-binding
328      Trxpep
330 <400> SEQUENCE: 10
331 Cys Gly Pro Ala Lys Arg Ala Asp Val Glu Phe Ser Leu Glu Pro Gly
332  1      5      10      15
335 <210> SEQ ID NO: 11
336 <211> LENGTH: 21
337 <212> TYPE: PRT
338 <213> ORGANISM: Artificial Sequence
340 <220> FEATURE:
341 <223> OTHER INFORMATION: Description of Artificial Sequence:CD40-binding
342      Trxpep

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 08/15/2005  
PATENT APPLICATION:    US/09/526,106B      TIME: 09:35:26

Input Set : A:\021167-000700US.ST25.txt  
Output Set: N:\CRF4\08152005\I526106B.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1

**VERIFICATION SUMMARY**

**PATENT APPLICATION: US/09/526,106B**

**DATE: 08/15/2005**

**TIME: 09:35:26**

**Input Set : A:\021167-000700US.ST25.txt**

**Output Set: N:\CRF4\08152005\I526106B.raw**